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In re Patent Application of:
Markus Matuschek et al.

Application No.: 10/521,916

Confirmation No.: N/A

Filed: January 20, 2005

Art Unit: N/A

For: PROCESS FOR THE BIOTRANSFORMATION
OF CAROTENOIDS

Examiner: Not Yet Assigned

**STATEMENT TO SUPPORT FILING AND SUBMISSION
IN ACCORDANCE WITH 37 CFR §§1.821 THROUGH 1.825**

MS Sequence
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

- I hereby state, in accordance with the requirements of 37 C.F.R. §1.821(f), that the information recorded in computer readable form is identical to the written Sequence Listing submitted herewith.
- I hereby state that the submission filed in accordance with 37 C.F.R. 1.821(g) does not include new matter.
- I hereby state that the submission filed in accordance with 37 C.F.R. §1.821(h) does not include new matter or go beyond the disclosure in the international application as filed.
- I hereby state that the amendments, made in accordance with 37 C.F.R. §1.825(a), included in the substitute sheet(s) of the Sequence Listing are supported in the application, as filed, in pages 1-11 of the Sequence Listing. I hereby state that the substitute sheets of the Sequence Listing do not include new matter.
- I hereby state that the substitute copy of the computer readable form, submitted in accordance with 37 C.F.R. §1.825(b), is the same as the amended Sequence Listing.
- I hereby state that the substitute copy of the computer readable form, submitted in accordance with 37 C.F.R. §1.825(d), contains identical data to that originally filed on January 20, 2005.

Dated: *April 26, 2005*

Respectfully submitted,

By Christine M. Hansen

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SEQUENCE LISTING

<110> Matuschek, Markus

Hauer, Bernhard

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Blasco, Francesca

Schmidt-Dannert, Claudia

<120> Process for the biotransformation of carotenoids

<130> 13111-00001-US

<140> 10/521,916

<141> 2005-01-20

<150> PCT/EP2003/008199

<151> 2003-07-25

<150> DE 102 34 126.5

<151> 2002-07-26

<160> 12

<170> PatentIn Ver. 3.3

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<211> 1170

<212> DNA

<213> Thermus thermophilus

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<221> CDS

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Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro
20 25 30

cgg ctc ttc ctt ccc ctg ccc cgc ttc ccc ctg gcc ctg atc ttt gac 144
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Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu	
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245 250 255	
gcc ttc cag gag gcc ctg agg ctc tac ccc ccc gcc tgg atc ctc acc	816
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260 265 270	
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Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro	
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Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys				
325	330	335		
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Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp				
35	40	45		
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Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu				
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85	90	95		
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 115 120 125
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 130 135 140
 Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala
 145 150 155 160
 Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp
 165 170 175
 Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg
 180 185 190
 Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg
 195 200 205
 Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu
 210 215 220
 Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg
 225 230 235 240
 Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala
 245 250 255
 Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr
 260 265 270
 Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro
 275 280 285
 Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe
 290 295 300
 Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly
 305 310 315 320
 Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys
 325 330 335
 Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala
 340 345 350
 Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu
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 Glu Glu Val Arg Ala
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 <223> His tag
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 his tagged
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 ccc tac ctg aaa gac ctc cag caa gat ccc ctc gcc gtc ctg ctg gcg 96
 Pro Tyr Leu Lys Asp Leu Gln Gln Asp Pro Leu Ala Val Leu Leu Ala
 20 25 30
 tgg ggc cgg gcc cac ccc cgg ctc ttc ctt ccc ctg ccc cgc ttc ccc 144
 Trp Gly Ala His Pro Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro
 35 40 45
 ctg gcc ctg atc ttt gac ccc gag ggg gtg gag ggg gcg ctc ctc gcc 192
 Leu Ala Leu Ile Phe Asp Pro Glu Gly Val Glu Gly Ala Leu Leu Ala
 50 55 60
 gag ggg acc acc aag gcc acc ttc cag tac cgg gcc ctc tcc cgc ctc 240
 Glu Gly Thr Thr Lys Ala Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu
 65 70 75 80
 acg ggg agg ggc ctc ctc acc gac tgg ggg gaa agc tgg aag gag gcg 288
 Thr Gly Arg Gly Leu Leu Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala
 85 90 95
 cgc aag gcc ctc aaa gac ccc ttc ctg ccg aag aac gtc cgc ggc tac 336
 Arg Lys Ala Leu Lys Asp Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr
 100 105 110
 cgg gag gcc atg gag gag gag gcc cgg gcc ttc ttc ggg gag tgg cgg 384
 Arg Glu Ala Met Glu Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg

115	120	125	
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130	135	140	
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145	150	155	160
gag cac gcc ctt aag gcc ctg gac cgg atc atg gcc cag acc agg agc Glu His Ala Leu Lys Ala Leu Asp Arg Ile Met Ala Gln Thr Arg Ser			528
165	170	175	
ccc ctg gcc ctc ctg gac ctg gcc gaa gcc cgc ttc cgg aag gac Pro Leu Ala Leu Leu Asp Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp			576
180	185	190	
cg ^g ggg gcc ctc tac cgc gag g ^c g gaa gcc ctc atc gtc cac cc ^g ccc Arg Gly Ala Leu Tyr Arg Glu Ala Glu Ala Leu Ile Val His Pro Pro			624
195	200	205	
ctc tcc cac ctt ccc cga gag cgc gcc ctg agc gag gcc gtg acc ctc Leu Ser His Leu Pro Arg Glu Arg Ala Leu Ser Glu Ala Val Thr Leu			672
210	215	220	
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225	230	235	240
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245	250	255	
gag gag g ^c g gcc ctc gcc ttc cag gag gcc ctg agg ctc tac ccc Glu Glu Ala Ala Leu Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro			816
260	265	270	
ccc gcc tgg atc ctc acc cc ^g agg ctg gaa agg ccc ctc ctc ctg gga Pro Ala Trp Ile Leu Thr Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly			864
275	280	285	
gag gac cc ^g ctc ccc cc ^g ggc acc acc ctg gtc ctc tcc ccc tac gtg Glu Asp Arg Leu Pro Pro Gly Thr Thr Leu Val Leu Ser Pro Tyr Val			912
290	295	300	
acc cag agg ctc cac ttc ccc gat ggg gag gcc ttc cc ^g ccc gag cgc Thr Gln Arg Leu His Phe Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg			960
305	310	315	320
ttc ctg gag gaa agg ggg acc cct tcg ggg cgc tac ttc ccc ttt ggc Phe Leu Glu Glu Arg Gly Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly			1008
325	330	335	
ctg ggg cag agg ctc tgc ctg ggg cc ^g gac ttc gcc ctc ctc gag ggc Leu Gly Gln Arg Leu Cys Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly			1056
340	345	350	

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 355 360 365

ccc ttc ccc cgg gtc ctc gcc cag gtc acc ctg agg ccc gaa ggc ggg 1152
 Pro Phe Pro Arg Val Leu Ala Gln Val Thr Leu Arg Pro Glu Gly Gly
 370 375 380

ctt ccc gcg cgg cct agg gag gag gtg cgg gcg tga 1188
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<211> 395

<212> PRT

<213> Artificial sequence

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 his tagged

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Trp Gly Arg Ala His Pro Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro
 35 40 45

Leu Ala Leu Ile Phe Asp Pro Glu Gly Val Glu Gly Ala Leu Leu Ala
 50 55 60 80

Glu Gly Thr Thr Lys Ala Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu
 65 70 75 80

Thr Gly Arg Gly Leu Leu Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala
 85 90 95

Arg Lys Ala Leu Lys Asp Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr
 100 105 110

Arg Glu Ala Met Glu Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg
 115 120 125

Gly Glu Glu Arg Asp Leu Asp His Glu Met Leu Ala Leu Ser Leu Arg
 130 135 140

Leu Leu Gly Arg Ala Leu Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala
 145 150 155 160

Glu His Ala Leu Lys Ala Leu Asp Arg Ile Met Ala Gln Thr Arg Ser
 165 170 175
 Pro Leu Ala Leu Leu Asp Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp
 180 185 190
 Arg Gly Ala Leu Tyr Arg Glu Ala Glu Ala Leu Ile Val His Pro Pro
 195 200 205
 Leu Ser His Leu Pro Arg Glu Arg Ala Leu Ser Glu Ala Val Thr Leu
 210 215 220
 Leu Val Ala Gly His Glu Thr Val Ala Ser Ala Leu Thr Trp Ser Phe
 225 230 235 240
 Leu Leu Leu Ser His Arg Pro Asp Trp Gln Lys Arg Val Ala Glu Ser
 245 250 255
 Glu Glu Ala Ala Leu Ala Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro
 260 265 270
 Pro Ala Trp Ile Leu Thr Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly
 275 280 285
 Glu Asp Arg Leu Pro Pro Gly Thr Thr Leu Val Leu Ser Pro Tyr Val
 290 295 300
 Thr Gln Arg Leu His Phe Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg
 305 310 315 320
 Phe Leu Glu Glu Arg Gly Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly
 325 330 335
 Leu Gly Gln Arg Leu Cys Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly
 340 345 350
 Pro Ile Val Leu Arg Ala Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu
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 370 375 380
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<210> 5

<211> 1188

<212> DNA

<213> Artificial sequence

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<221> misc_feature

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His-tagged

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Gln	Gln	Asp	Pro	Leu	Ala	Val	Leu	Leu	Ala	Trp	Gly	Arg	Ala	His	Pro	
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Pro	Glu	Gly	Val	Glu	Gly	Ala	Leu	Leu	Ala	Glu	Gly	Thr	Thr	Lys	Ala		
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acc	ttc	cag	tac	cg	gcc	ctc	tcc	cgc	ctc	acg	ggg	agg	ggc	ctc	ctc	240
Thr	Phe	Gln	Tyr	Arg	Ala	Leu	Ser	Arg	Leu	Thr	Gly	Arg	Gly	Leu	Leu	
65				70						75			80			

acc	gac	tgg	ggg	gaa	agc	tgg	aag	gag	g	c	gc	aag	gcc	ctc	aaa	gac	288
Thr	Asp	Trp	Gly	Glu	Ser	Trp	Lys	Glu	Ala	Arg	Lys	Ala	Leu	Lys	Asp		
85				90								95					

ccc	ttc	ctg	ccg	aag	aa	gtc	cgc	ggc	tac	cg	gag	gg	cc	at	g	gag	336
Pro	Phe	Leu	Pro	Lys	Asn	Val	Arg	Gly	Tyr	Arg	Glu	Ala	Met	Glu	Glu		
100				105								110					

gag	gcc	cg	gg	ttc	ttc	gg	gag	tgg	cg	gg	gag	gag	cg	gac	ct	384	
Glu	Ala	Arg	Ala	Phe	Phe	Gly	Glu	Trp	Arg	Gly	Glu	Glu	Arg	Asp	Leu		
115				120								125					

gac	cac	gag	at	g	ct	g	cc	ct	ct	cg	gg	cc	cc	ct	432		
Asp	His	Glu	Met	Leu	Ala	Leu	Ser	Leu	Arg	Leu	Leu	Gly	Arg	Ala	Leu		
130				135								140					

ttc	gg	a	cc	ct	tcc	cc	ag	ct	g	cg	g	ac	cc	tt	a	gg	480
Phe	Gly	Lys	Pro	Leu	Ser	Pro	Ser	Leu	Ala	Glu	His	Ala	Leu	Lys	Ala		

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ctg gac cgg atc atg gcc cag acc agg agc ccc ctg gcc ctc ctg gac Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp				528
165		170		175
ctg gcc gaa gcc cgc ttc cgg aag gac cgg ggg gcc ctc tac cgc Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg				576
180		185		190
gag gcg gaa gcc ctc atc gtc cac ccc ctc tcc cac ctt ccc cga Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg				624
195		200		205
gag cgc gcc ctg agc gag gcc gtg acc ctc ctg gtg gcg ggc cac gag Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu				672
210		215		220
acg gtg gcg agc gcc ctc acc tgg tcc ttt ctc ctc tcc cac cgc Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg				720
225		230		235
				240
ccg gac tgg cag aag cgg gtg gcc gag agc gag gag gcg gcc ctc gcc Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala				768
245		250		255
gcc ttc cag gag gcc ctg agg ctc tac ccc ccc gcc tgg atc ctc acc Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr				816
260		265		270
cgg agg ctg gaa agg ccc ctc ctc ctg gga gag gac cgg ctc ccc ccg Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro				864
275		280		285
ggc acc acc ctg gtc ctc tcc ccc tac gtg acc cag agg ctc cac ttc Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe				912
290		295		300
ccc gat ggg gag gcc ttc cgg ccc gag cgc ttc ctg gag gaa agg ggg Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly				960
305		310		315
				320
acc cct tcg ggg cgc tac ttc ccc ttt ggc ctg ggg cag agg ctc tgc Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys				1008
325		330		335
ctg ggg cgg gac ttc gcc ctc ctc gag ggc ccc atc gtc ctc agg gcc Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala				1056
340		345		350
ttc ttc cgc cgc ttc cgc cta gac ccc ctc ccc ttc ccc cgg gtc ctc Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu				1104
355		360		365
gcc cag gtc acc ctg agg ccc gaa ggc ggg ctt ccc gcg cgg cct agg Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg				1152
370		375		380

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 Glu Glu Val Arg Ala His His His His His His His
 385 390 395

<210> 6

<211> 395

<212> PRT

<213> Artificial sequence

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<223> Description of the artificial sequence: C-terminal
His-tagged

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Met Lys Arg Leu Ser Leu Arg Glu Ala Trp Pro Tyr Leu Lys Asp Leu
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Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro
20 25 30

Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp
35 40 45

Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala
50 55 60

Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu
65 70 75 80

Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp
85 90 95

Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu
100 105 110

Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu
115 120 125

Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu
130 135 140

Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala
145 150 155 160

Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp
165 170 175

Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg
180 185 190

Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg

195	200	205
Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu		
210	215	220
Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg		
225	230	235
240		
Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala		
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Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr		
260	265	270
Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro		
275	280	285
Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe		
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Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly		
305	310	315
320		
Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys		
325	330	335
Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala		
340	345	350
Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu		
355	360	365
Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg		
370	375	380
Glu Glu Val Arg Ala His His His His His His		
385	390	395

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<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 7

cgaagctcat atgaagcgcc tttccctgag

30

<210> 8

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<220>
<223> Description of the artificial sequence: PCR primer

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<210> 9
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<212> DNA
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<223> Description of the artificial sequence: PCR primer

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<210> 11
<211> 30
<212> DNA
<213> Artificial sequence
<220>

<223> Description of the artificial sequence: PCR primer

<400> 11

ccggaattca tgaagcgctt tccctgagg

30

<210> 12

<211> 44

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

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44